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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=10; day=29; hr=10; min=16; sec=23; ms=374;  
]

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Application No: 10543046 Version No: 2.0

Input Set:

Output Set:

Started: 2008-09-29 14:31:17.151  
Finished: 2008-09-29 14:31:17.550  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 399 ms  
Total Warnings: 5  
Total Errors: 0  
No. of SeqIDs Defined: 5  
Actual SeqID Count: 5

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)

# SEQUENCE LISTING

<110> Shewchuk, Lisa Marie  
 Hassell, Anne Moore  
 Brignola, Perry Scott

<120> ERB4 Co-Crystal

<130> PU4804USw

<140> 10543046

<141> 2005-07-21

<150> PCT/US04/01291

<151> 2004-01-20

<150> US 60/441,443

<151> 2003-01-21

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 364

<212> PRT

<213> Homo sapein

<400> 1

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Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Thr	Ala	Pro	Asn	Gln	Ala	Gln	Leu
			20					25					30		
Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	Lys	Arg	Val	Lys	Val	Leu	Gly	Ser
		35					40					45			
Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Ile	Trp	Val	Pro	Glu	Gly	Glu
	50					55				60					
Thr	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Ile	Leu	Asn	Glu	Thr	Thr	Gly
65					70					75					80
Pro	Lys	Ala	Asn	Val	Glu	Phe	Met	Asp	Glu	Ala	Leu	Ile	Met	Ala	Ser
			85						90					95	
Met	Asp	His	Pro	His	Leu	Val	Arg	Leu	Leu	Gly	Val	Cys	Leu	Ser	Pro
			100						105					110	
Thr	Ile	Gln	Leu	Val	Thr	Gln	Leu	Met	Pro	His	Gly	Cys	Leu	Leu	Glu
		115					120					125			
Tyr	Val	His	Glu	His	Lys	Asp	Asn	Ile	Gly	Ser	Gln	Leu	Leu	Leu	Asn
	130					135					140				
Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Met	Tyr	Leu	Glu	Glu	Arg	Arg
145					150					155					160
Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro
			165						170					175	
Asn	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Leu	Glu	Gly
		180						185						190	
Asp	Glu	Lys	Glu	Tyr	Asn	Ala	Asp	Gly	Gly	Lys	Met	Pro	Ile	Lys	Trp

195	200	205
Met Ala Leu Glu Cys Ile His Tyr Arg Lys Phe Thr His Gln Ser Asp		
210	215	220
Val Trp Ser Tyr Gly Val Thr Ile Trp Glu Leu Met Thr Phe Gly Gly		
225	230	235
Lys Pro Tyr Asp Gly Ile Pro Thr Arg Glu Ile Pro Asp Leu Leu Glu		
245	250	255
Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr		
260	265	270
Met Val Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys		
275	280	285
Phe Lys Glu Leu Ala Ala Glu Phe Ser Arg Met Ala Arg Asp Pro Gln		
290	295	300
Arg Tyr Leu Val Ile Gln Gly Asp Asp Arg Met Lys Leu Pro Ser Pro		
305	310	315
Asn Asp Ser Lys Phe Phe Gln Asn Leu Leu Asp Glu Glu Asp Leu Glu		
325	330	335
Asp Met Met Asp Ala Glu Glu Tyr Leu Val Pro Gln Ala Phe Asn Ile		
340	345	350
Pro Pro Pro Ile Tyr Thr Ser Arg Ala Arg Ile Asp		
355	360	

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 <213> Homo sapien

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 actcccagtg gcacagcacc caatcaagct caacttcgta ttttgaaaga aactgagctg 120  
 aagagggtaa aagtccttgg ctcaggtgct tttggaacgg tttataaagg tatttgggta 180  
 cctgaaggag aaactgtgaa gattcctgtg gctattaaga ttcttaatga gacaactggt 240  
 cccaaggcaa atgtggagtt catggatgaa gctctgatca tggcaagtat ggatcatcca 300  
 cacctagtcc gggttgcctggg tgtgtgtctg agcccaacca tccagctggt tactcaactt 360  
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 ctgctgctta actggtgtgt ccagatagct aagggaatga tgtacctgga agaaagacga 480  
 ctcggtcatc gggatttggc agcccgtaat gtcttagtga aatctccaaa ccatgtgaaa 540  
 atcacagatt ttgggctagc cagactcttg gaaggagatg aaaaagagta caatgctgat 600  
 ggaggaaaga tgccaattaa atggatggct ctggagtgtg tacattacag gaaattcacc 660  
 catcagagtg acgtttggag ctatggagtt actatatggg aactgatgac ctttggagga 720  
 aaaccctatg atggaattcc aacgcgagaa atccctgatt tattagagaa aggagaacgt 780  
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 aattga 966

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 <213> Artificial Sequence

<220>  
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 coordinates are shown in Table 2

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Ala	Glu	Thr	Glu	Leu	Ala	Arg	Val	Ala	Val	Leu	Gly	Ser	Gly	Ala	Phe	20	25	30	
Gly	Thr	Val	Tyr	Lys	Gly	Ile	Trp	Val	Pro	Ala	Gly	Glu	Ala	Val	Lys	35	40	45	
Ile	Pro	Val	Ala	Ile	Lys	Ile	Ala	Val	Ala	Asn	Val	Glu	Phe	Met	Asp	50	55	60	
Glu	Ala	Leu	Ile	Met	Ala	Ser	Met	Asp	His	Pro	His	Leu	Val	Arg	Leu	65	70	75	80
Leu	Gly	Val	Cys	Leu	Ser	Pro	Thr	Ile	Gln	Leu	Val	Thr	Gln	Leu	Met	85	90	95	
Pro	His	Gly	Cys	Leu	Leu	Glu	Tyr	Val	His	Glu	His	Lys	Asp	Asn	Ile	100	105	110	
Gly	Ser	Gln	Leu	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	115	120	125	
Met	Tyr	Leu	Glu	Glu	Arg	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	130	135	140	
Asn	Val	Leu	Val	Lys	Ser	Pro	Ala	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	145	150	155	160
Leu	Ala	Arg	Leu	Leu	Glu	Gly	Asp	Glu	Lys	Glu	Tyr	Asn	Ala	Asp	Gly	165	170	175	
Gly	Lys	Met	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Cys	Ile	His	Tyr	Arg	180	185	190	
Ala	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Ile	Trp	195	200	205	
Glu	Leu	Met	Thr	Phe	Gly	Gly	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Thr	Ala	210	215	220	
Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro	Pro	225	230	235	240
Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Val	Met	Val	Lys	Cys	Trp	Met	Ile	245	250	255	
Asp	Ala	Asp	Ser	Arg	Pro	Lys	Phe	Ala	Glu	Leu	Ala	Ala	Glu	Phe	Ser	260	265	270	
Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Tyr	Leu	Val	Ile	Gln	Gly	Asp	Ala	275	280	285	
Ala	Ala	Ala	Ala	Pro	Leu	Thr	Pro	Ser	Gly	Thr	Ala	Pro	Asn	Gln	Ala	290	295	300	
Gln	Leu	Arg	Ile	Leu	Ala	Glu	Thr	Glu	Leu	Ala	Arg	Val	Ala	Val	Leu	305	310	315	320
Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Ile	Trp	Val	Pro	Ala	325	330	335	
Gly	Glu	Ala	Val	Ala	Ile	Pro	Val	Ala	Ile	Lys	Ile	Ala	Val	Ala	Ala	340	345	350	
Asn	Val	Ala	Phe	Met	Asp	Glu	Ala	Leu	Ile	Met	Ala	Ser	Met	Asp	His	355	360	365	
Pro	His	Leu	Val	Arg	Leu	Leu	Gly	Val	Cys	Leu	Ser	Pro	Thr	Ile	Gln	370	375	380	
Leu	Val	Thr	Gln	Leu	Met	Pro	His	Gly	Cys	Leu	Leu	Glu	Tyr	Val	His	385	390	395	400
Glu	His	Lys	Asp	Asn	Ile	Gly	Ser	Gln	Leu	Leu	Leu	Asn	Trp	Cys	Val	405	410	415	
Gln	Ile	Ala	Lys	Gly	Met	Met	Tyr	Leu	Glu	Glu	Arg	Arg	Leu	Val	His	420	425	430	
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Ala	His	Val	435	440	445	
Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Leu	Glu	Gly	Asp	Glu	Ala				

450		455		460
Ala Tyr Asn Ala Asp Gly Gly Ala Met Pro Ile Lys Trp Met Ala Leu				
465		470		475
Glu Cys Ile His Tyr Arg Ala Phe Thr His Gln Ser Asp Val Trp Ser				
	485		490	495
Tyr Gly Val Thr Ile Trp Glu Leu Met Thr Phe Gly Lys Pro Tyr Asp				
	500		505	510
Gly Ile Pro Thr Ala Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg				
	515		520	525
Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Val Met Val				
	530		535	540
Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Ala Glu Leu				
545		550		555
Ala Ala Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Tyr Leu Val				
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Ile Gln Gly Asp Ala				
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> His tag for Erb4 cytoplasmic domain

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<210> 5  
 <211> 15  
 <212> PRT  
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<220>  
 <223> Substrate peptide for Erb4 activity assay

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 1 5 10 15